

In the specification:

Please replace the paragraph on page 11, lines 9-25, of the specification with the following paragraph.

Twenty amino acids were identified as highly conserved (shown as the shaded residues in Fig. 1). The percent of RNase P sequences which conserve each of the shaded residues is shown below the sequence information as percent identity. Based upon these known sequences, we determined that a polypeptide identified by our above-described RNase P BLAST search contained an RNase P consensus sequence and was a genuine RNase P protein subunit if it contained at least nine of the above-described twenty amino acids. Preferred polypeptides have a consensus sequence with at least 13 of the amino acids and/or conserve at least seven of the following subset of amino acids: F18, R46, K53, A59, R62, N63, K66, R67, and R70. This subset of amino acids is preferred because it has been identified as playing a significant role in RNase P function through mutation studies (Gopalan et al., J. Mol. Biol. 267: 818 1997) and the determination of the RNase P three dimensional structure (Stains ~~Stams~~ et al., Science 280: 752, 1998). ~~As shown in Fig. 2, the~~ The three dimensional structure reveals that all of the residues that make up the above-described nine amino acid subset are proximal to each other in the tertiary structure of the protein, despite the distance between some of the residues in the primary structure.